Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:07:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068934.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6068934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:07:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,653,976
Mapped reads	1,053,562 / 63.7%
Unmapped reads	600,414 / 36.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,371 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	166,153 / 10.05%
Duplication rate	12.22%
Clipped reads	667,027 / 40.33%

2.2. ACGT Content

Number/percentage of A's	17,252,024 / 26.32%
Number/percentage of C's	12,441,296 / 18.98%
Number/percentage of T's	20,460,774 / 31.22%
Number/percentage of G's	15,369,048 / 23.45%
Number/percentage of N's	12,078 / 0.02%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2815

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

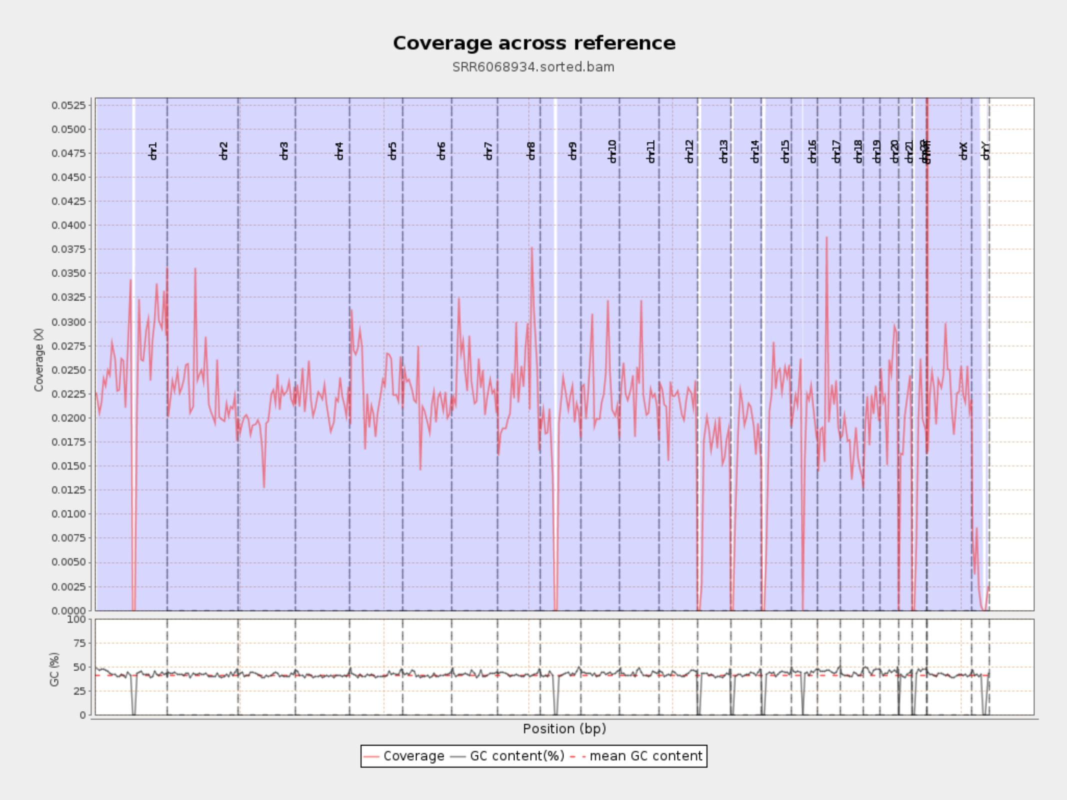
General error rate	1.04%
Mismatches	676,072
Insertions	5,097
Mapped reads with at least one insertion	0.48%
Deletions	21,292
Mapped reads with at least one deletion	2%
Homopolymer indels	46.96%

2.6. Chromosome stats

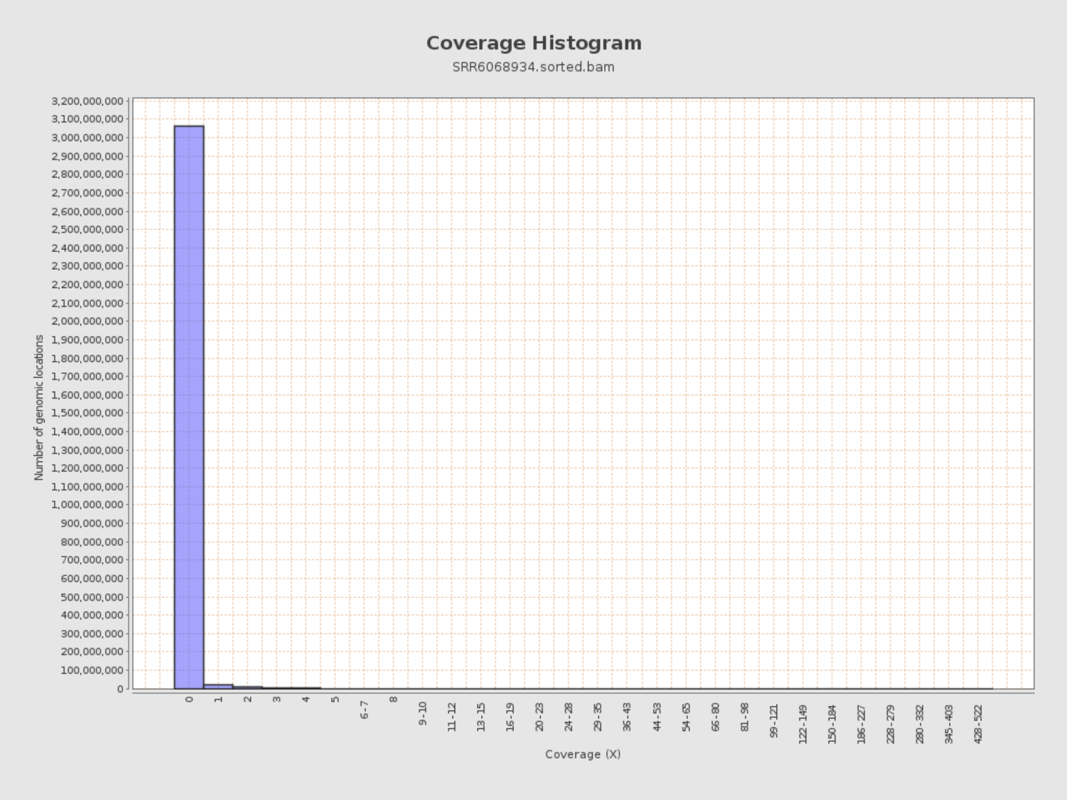
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6226875	0.025	0.358
chr2	243199373	5554663	0.0228	0.2951
chr3	198022430	4049336	0.0204	0.2428
chr4	191154276	4194024	0.0219	0.2508
chr5	180915260	4320479	0.0239	0.2635
chr6	171115067	3690171	0.0216	0.2745
chr7	159138663	3807669	0.0239	0.305

chr8	146364022	3462759	0.0237	0.2739
chr9	141213431	2576294	0.0182	0.2405
chr10	135534747	3109873	0.0229	0.4322
chr11	135006516	3106735	0.023	0.2767
chr12	133851895	2896586	0.0216	0.2486
chr13	115169878	1717624	0.0149	0.2101
chr14	107349540	1759187	0.0164	0.2286
chr15	102531392	1983536	0.0193	0.2412
chr16	90354753	1750546	0.0194	0.24
chr17	81195210	1724684	0.0212	0.2505
chr18	78077248	1317659	0.0169	0.2822
chr19	59128983	1198420	0.0203	0.2928
chr20	63025520	1501472	0.0238	0.2683
chr21	48129895	861169	0.0179	0.2319
chr22	51304566	740307	0.0144	0.2013
chrMT	16571	277955	16.7736	11.6529
chrX	155270560	3564755	0.023	0.2574
chrY	59373566	175684	0.003	0.0879

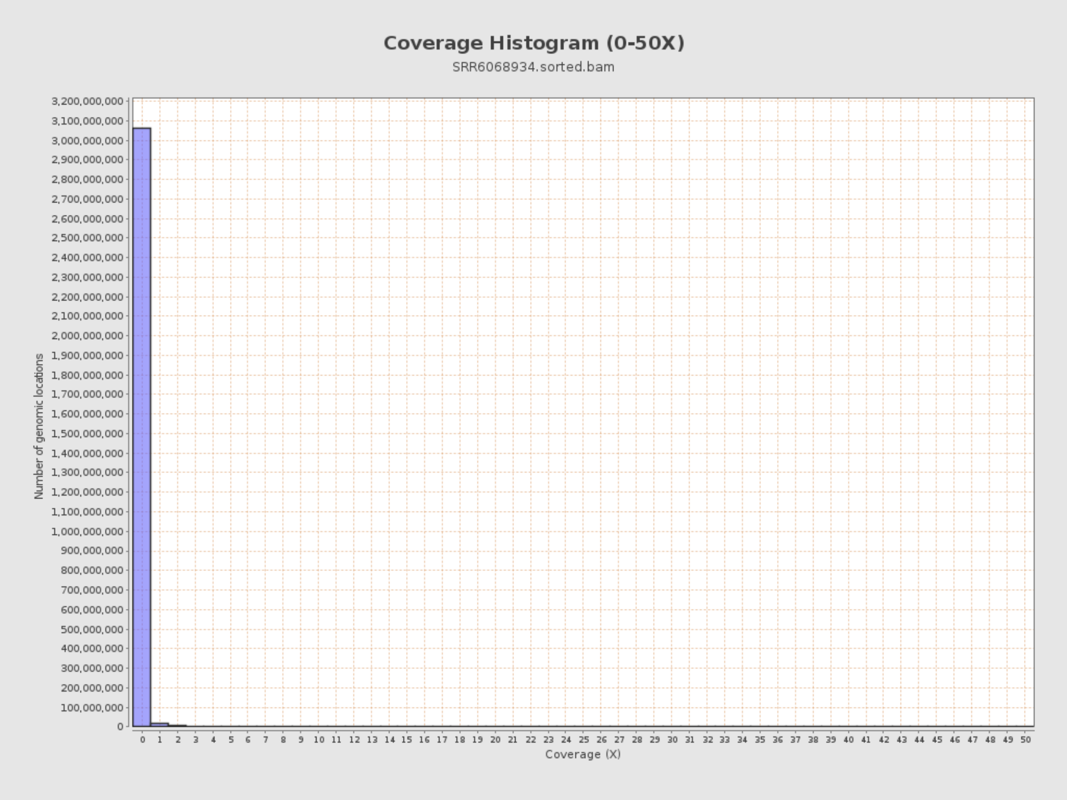
3. Results : Coverage across reference



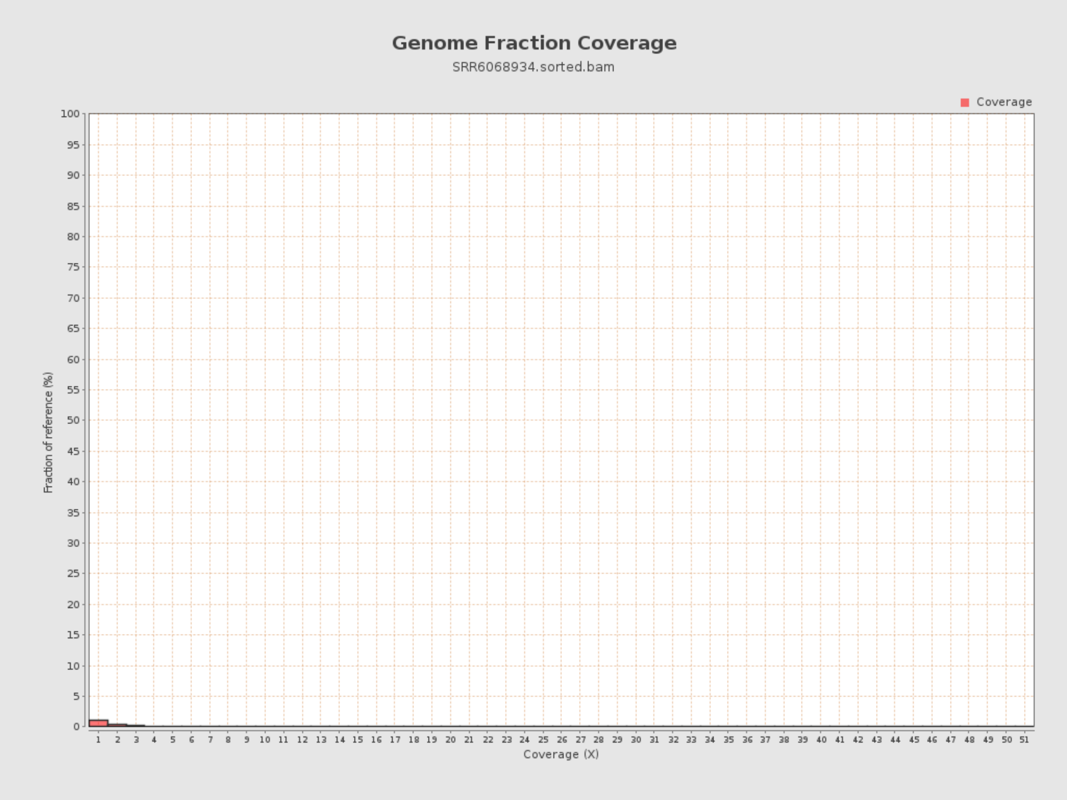
4. Results : Coverage Histogram



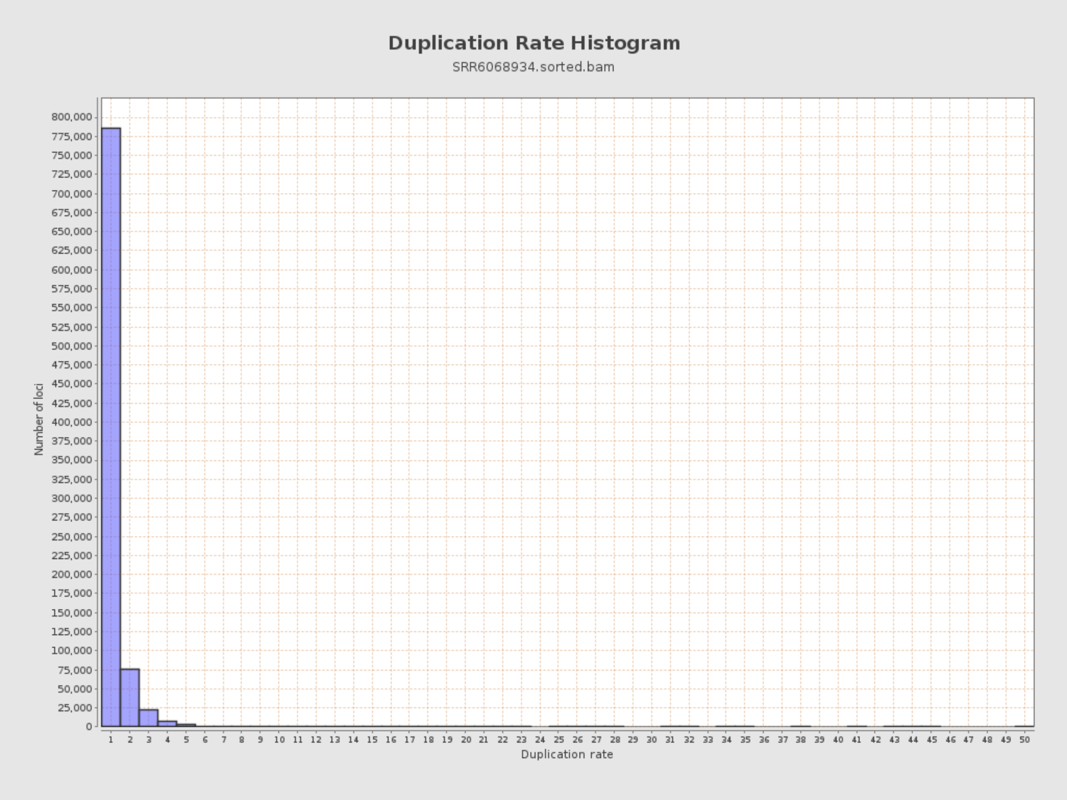
5. Results : Coverage Histogram (0-50X)



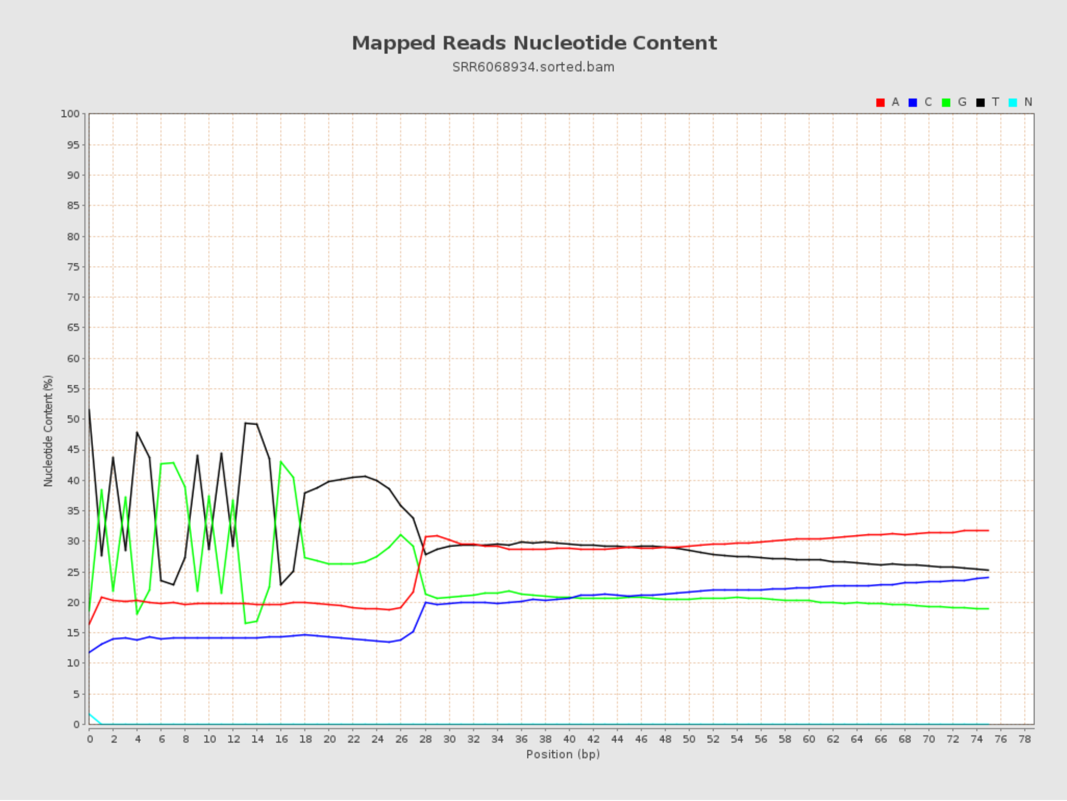
6. Results : Genome Fraction Coverage



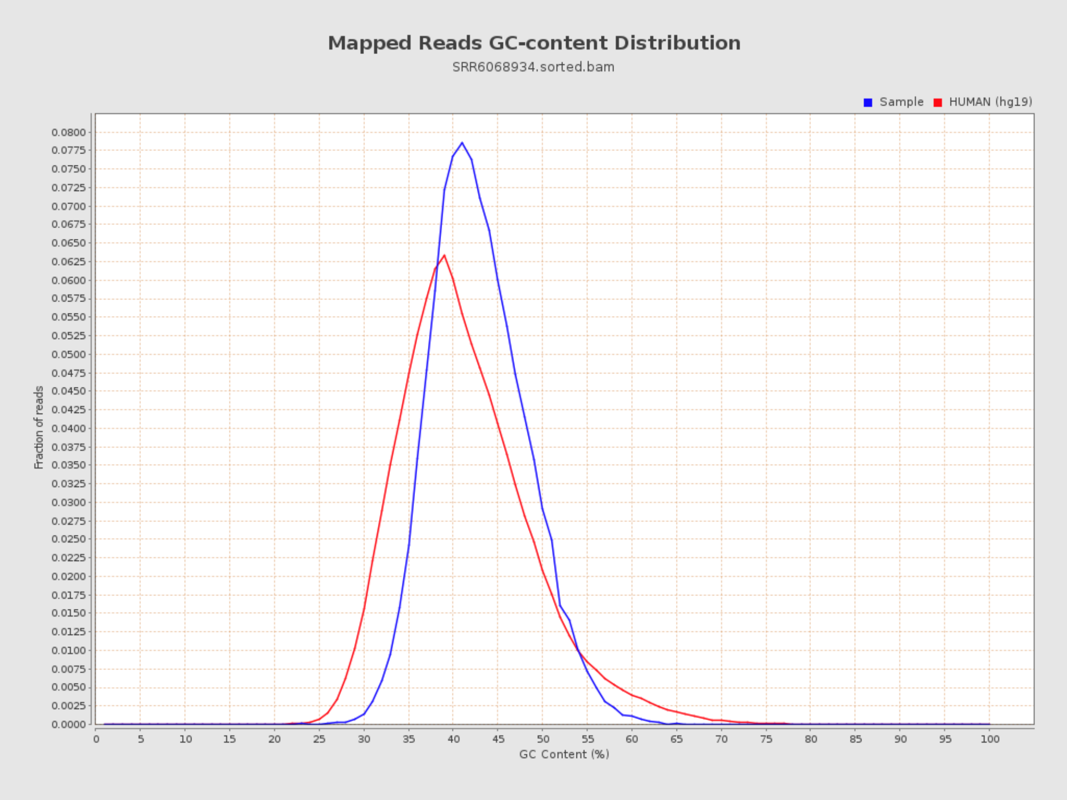
7. Results : Duplication Rate Histogram



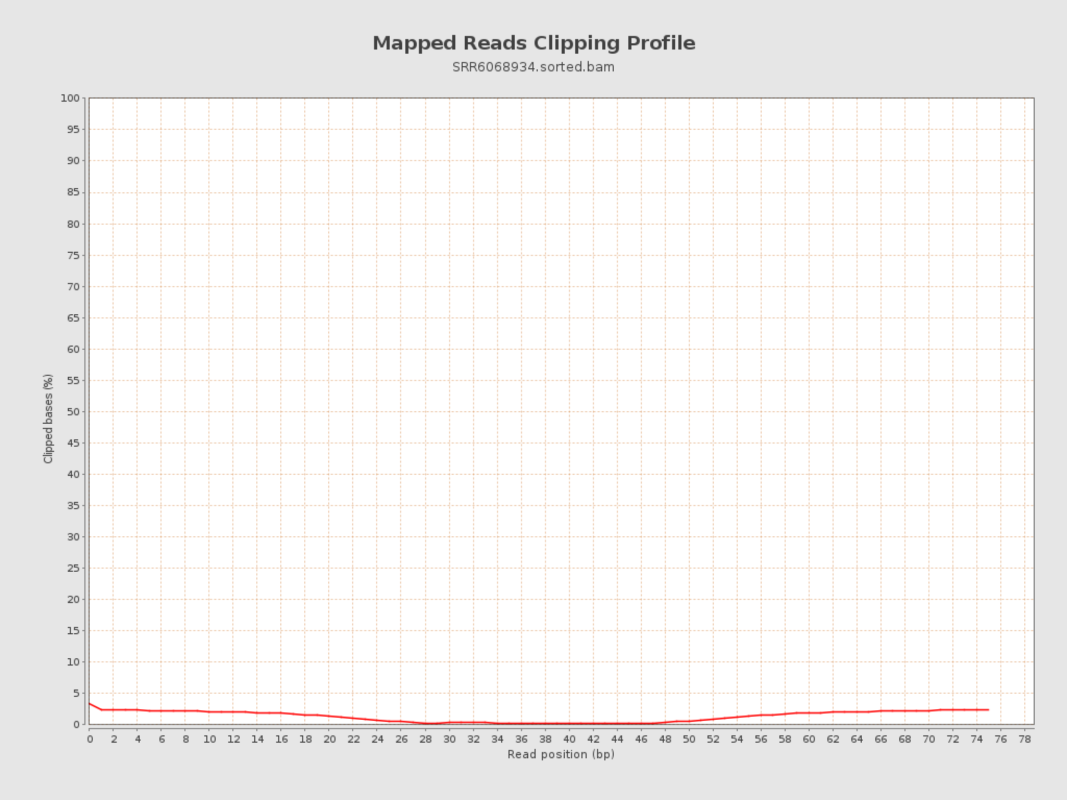
8. Results : Mapped Reads Nucleotide Content



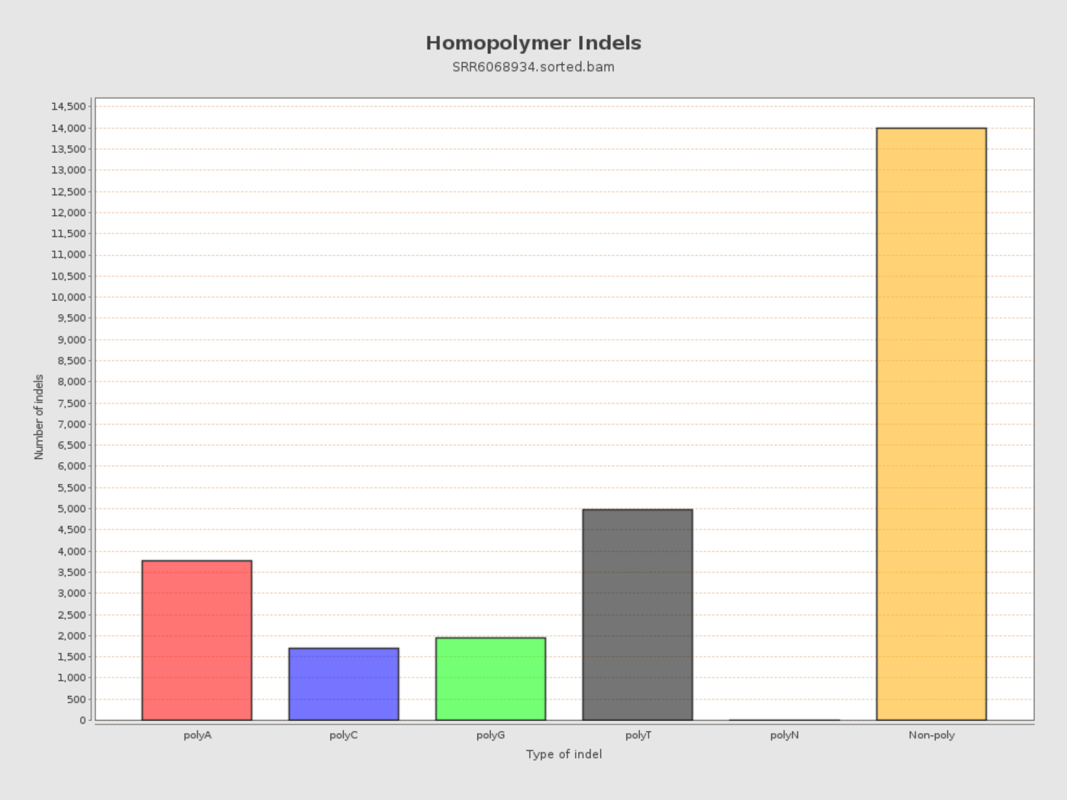
9. Results : Mapped Reads GC-content Distribution



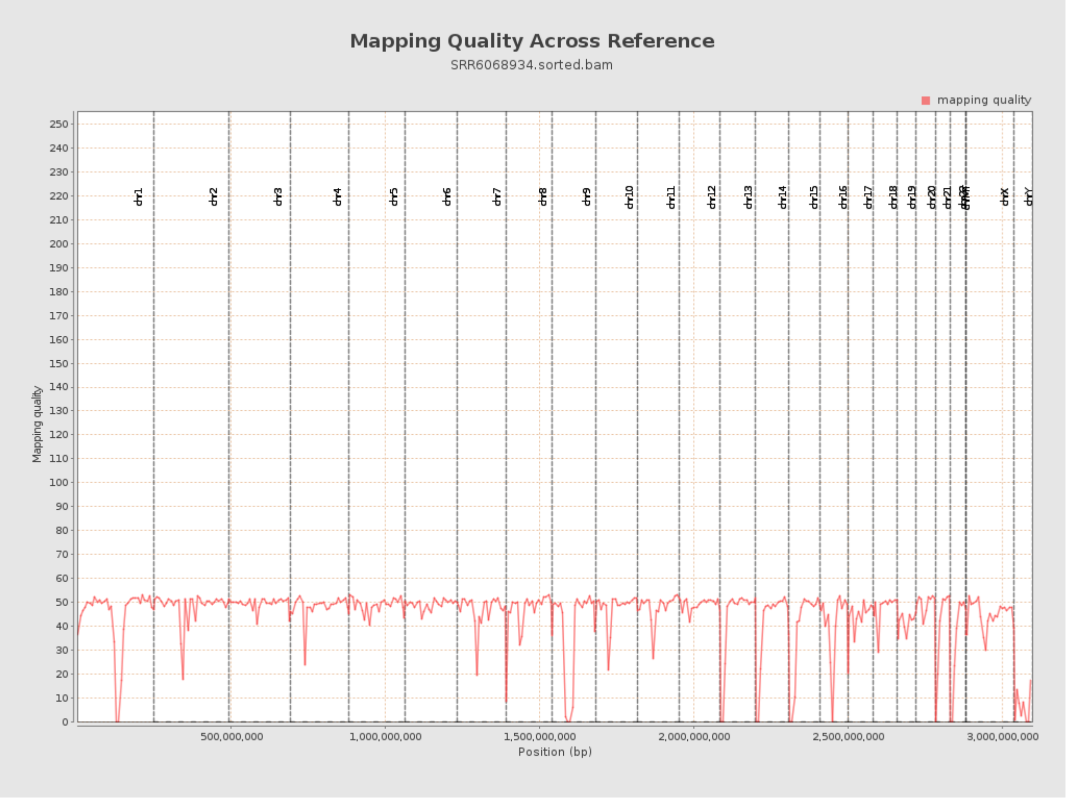
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram